



1600

## RAW SEQUENCE LISTING

DATE: 04/08/2003

PATENT APPLICATION: US/09/859,701

TIME: 12:16:44

Input Set : A:\94661sequencelisting.ST25.txt

Output Set: N:\CRF4\04082003\I859701.raw

3 <110> APPLICANT: Warner, Benjamin P  
 5 <120> TITLE OF INVENTION: Method for Detecting Binding Events Using Micro-X-Ray  
 6 Fluorescence Spectrometry  
 8 <130> FILE REFERENCE: S-94,661  
 10 <140> CURRENT APPLICATION NUMBER: 09/859,701  
 11 <141> CURRENT FILING DATE: 2001-05-16  
 13 <160> NUMBER OF SEQ ID NOS: 5  
 15 <170> SOFTWARE: PatentIn version 3.2  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 11  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: artificial sequence  
 22 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Xaa can be His, Arg, Ser, Trp, or Tyr  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: MISC\_FEATURE  
 28 <222> LOCATION: (1)..(11)  
 29 <223> OTHER INFORMATION: X can be H, R, S, W, or Y  
 31 <400> SEQUENCE: 1  
 W--> 33 Xaa Gly Gly Xaa Gly Gly Xaa Gly Phe  
 34 1 5 10  
 37 <210> SEQ ID NO: 2  
 38 <211> LENGTH: 11  
 39 <212> TYPE: PRT  
 40 <213> ORGANISM: artificial sequence  
 42 <220> FEATURE:  
 43 <223> OTHER INFORMATION: binds strongly to methylphosphonic acid  
 46 <220> FEATURE:  
 47 <221> NAME/KEY: BINDING  
 48 <222> LOCATION: (1)..(11)  
 50 <400> SEQUENCE: 2  
 52 His Gly Gly His Gly Gly His Gly Arg Phe  
 53 1 5 10  
 56 <210> SEQ ID NO: 3  
 57 <211> LENGTH: 11  
 58 <212> TYPE: PRT  
 59 <213> ORGANISM: artificial sequence  
 61 <220> FEATURE:  
 62 <223> OTHER INFORMATION: binds strongly to methylphosphonic acid  
 65 <220> FEATURE:  
 66 <221> NAME/KEY: BINDING  
 67 <222> LOCATION: (1)..(11)  
 69 <400> SEQUENCE: 3

pp1-2  
 Does Not Comply  
 Corrected Diskette Needed

needs to be explained in <2207-2237  
 section.

see item 11  
 on Error summary  
 sheet

FYI: explain source of genetic  
 material  
 in <2207-2237  
 section

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71 Tyr Gly Gly Tyr Gly Gly Trp Gly Gly Tyr Phe

72 1 5 10

75 &lt;210&gt; SEQ ID NO: 4

76 &lt;211&gt; LENGTH: 11

77 &lt;212&gt; TYPE: PRT

78 &lt;213&gt; ORGANISM: artificial sequence

80 &lt;220&gt; FEATURE:

81 &lt;223&gt; OTHER INFORMATION: binds to the thiol

84 &lt;220&gt; FEATURE:

85 &lt;221&gt; NAME/KEY: BINDING

86 &lt;222&gt; LOCATION: (1)..(11)

88 &lt;400&gt; SEQUENCE: 4

90 Ser Gly Gly Arg Gly Gly His Gly Gly His Phe

91 1 5 10

94 &lt;210&gt; SEQ ID NO: 5

95 &lt;211&gt; LENGTH: 11

96 &lt;212&gt; TYPE: PRT

97 &lt;213&gt; ORGANISM: artificial sequence

99 &lt;220&gt; FEATURE:

100 &lt;223&gt; OTHER INFORMATION: binds to the thiol

103 &lt;220&gt; FEATURE:

104 &lt;221&gt; NAME/KEY: BINDING

105 &lt;222&gt; LOCATION: (1)..(11)

107 &lt;400&gt; SEQUENCE: 5

109 Trp Phe Phe His Gly Gly His Gly Gly Trp Phe

110 1 5 10

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 04/08/2003  
PATENT APPLICATION: US/09/859,701      TIME: 12:16:45

Input Set : A:\94661sequencelisting.ST25.txt  
Output Set: N:\CRF4\04082003\I859701.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,4,7,10

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/859,701

DATE: 04/08/2003

TIME: 12:16:45

Input Set : A:\94661sequencelisting.ST25.txt

Output Set: N:\CRF4\04082003\I859701.raw

L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/859,701

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (Sec. "Federal Register," 06/01/1998, Vol 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.